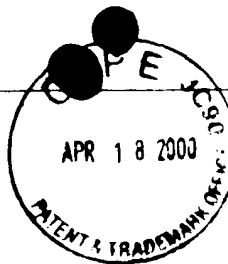


Sequence Listing

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Genentech, Inc., Hsei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
Presta, Leonard G.
Shahrokh, Zahra
Zapata, Gerardo A.
- (ii) TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
- (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/234182
 - (B) FILING DATE: 20-Jan-1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/074330
 - (B) FILING DATE: 22-JAN-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/094003
 - (B) FILING DATE: 24-JUL-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/094013
 - (B) FILING DATE: 24-JUL-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/075467
 - (B) FILING DATE: 20-FEB-1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Love, Richard B.
 - (B) REGISTRATION NUMBER: 34,659
 - (C) REFERENCE/DOCKET NUMBER: P1085R4-1A

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 650/225-5530
 (B) TELEFAX: 650/952-9881
(2) INFORMATION FOR SEQ ID NO:1:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTCCAACT GTTCAGGACG CC 22

(2) INFORMATION FOR SEQ ID NO:2:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCTGCTCA TGCTGTAGGT GC 22

(2) INFORMATION FOR SEQ ID NO:3:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTGATG TCTTGTGAGT GGC 23

(2) INFORMATION FOR SEQ ID NO:4:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCATCCTAGA GTCACCGAGG AGCC 24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGGCTCA GGGAAATAAC CC 22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGAGCTGG GAAGGTGTGC AC 22

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGC 37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGT TTTGGC 39

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGT TTTGGC 39

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGATGGGCCC GGATAGACTG ATGGGGCTGT TGT TTTGGC 39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50
CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100
CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150
TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200
TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250
CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300
GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350
CATCTTCCCA CCATTGAA 369

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val
 1             5             10             15
Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly
             20             25             30
Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
             35             40             45
Ala Leu Ile Tyr Ser Ser Ser Tyr Arg Tyr Ser Gly Val Pro Asp
             50             55             60
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
             65             70             75
Ser His Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
             80             85             90
Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Pro Gly Thr Lys Leu Glu
             95            100            105
Leu Lys Arg Ala Asp Ala Ala Pro Pro Thr Val Ser Ile Phe Pro
            110            115            120
Pro Phe Glu
  
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG 50
GAGGCTTAGT GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT 100
GGATTCATAT TCAGTAGTTA TGGCATGTCT TGGGTTCGCC AGACTCCAGG 150
CAAGAGCCTG GAGTTGGTCG CAACCATTA TAATAATGGT GATAGCACCT 200
ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250
AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300
  
```

CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT 350
 ACTGGGGCCA AGGGACTCTG GTCAGTGTCT CTGCAGCCAA AACAACAGCC 400
 CCATCTGTCT ATCCGGG 417

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Pro	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	20	25	30	
Ser	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Gly	Lys	Ser	Leu	35	40	45	
Glu	Leu	Val	Ala	Thr	Ile	Asn	Asn	Asn	Gly	Asp	Ser	Thr	Tyr	Tyr	50	55	60	
Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	65	70	75	
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	80	85	90	
Thr	Ala	Met	Phe	Tyr	Cys	Ala	Arg	Ala	Leu	Ile	Ser	Ser	Ala	Thr	95	100	105	
Trp	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	110	115	120	
Ala	Lys	Thr	Thr	Ala	Pro	Ser	Val	Tyr	Pro	125	130							

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCACTAGTAC GCAAGTTCAC G 21

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 714 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTTTCTAT 50
TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100
TGTCCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150
AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200
TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA GTCCCTGATC 250

GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300
 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTCAGCAAT ATAACATCTA 350
 TCCTCTCAGC TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGA3CTGTGG 400
 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450
 GGAAGTCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500
 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550
 AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600
 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650
 CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700
 GGGGAGAGTG TTAA 714

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	20	25	30	
Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Val	Thr	35	40	45	
Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	50	55	60	
Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr	Ser	Ser	Ser	65	70	75	
Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	80	85	90	
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	His	Val	Gln	Ser	Glu	Asp	95	100	105	
Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ile	Tyr	Pro	Leu	Thr	110	115	120	
Phe	Gly	Pro	Gly	Thr	Lys	Leu	Glu	Leu	Arg	Arg	Ala	Val	Ala	Ala	125	130	135	

Pro Ser Val Phe	Ile Phe Pro Pro Ser	Asp Glu Gln Leu Lys Ser	
	140	145	150
Gly Thr Ala Ser	Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg		
	155	160	165
Glu Ala Lys Val	Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly		
	170	175	180
Asn Ser Gln Glu	Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr		
	185	190	195
Tyr Ser Leu Ser	Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu		
	200	205	210
Lys His Lys Val	Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
	215	220	225
Ser Pro Val Thr	Lys Ser Phe Asn Arg Gly Glu Cys		
	230	235	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTTTCTAT 50
TGCTACAAAC GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT 100
TAGTGCCGCC TGGAGGGTCC CTGAAACTCT CCTGTGCAGC CTCTGGATTC 150
ATATTCA GTA GTTATGGCAT GTCTTGGGTT CGCCAGACTC CAGGCAAGAG 200
CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC ACCTATTATC 250
CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC 300
ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT 350
TTACTGTGCA AGAGCCCTCA TTAGTTCGGC TACTTGTTTT GGTTACTGGG 400
GCCAAGGGAC TCTGGTCACT GTCTCTGCAG CCTCCACCAA GGGCCCATCG 450
GTCTTCCCCC TGGCACCCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC 500
CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCTGT 550
GGAAGTCAAG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTTA 600
CAGTCTCAAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG 650

```

CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA 700

ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAACCTCAC 750

ACATGA 756

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
1				5					10					15	
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser	
			20					25					30		
Gly	Gly	Gly	Leu	Val	Pro	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	
			35					40					45		
Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	Ser	Trp	Val	
			50					55					60		
Arg	Gln	Thr	Pro	Gly	Lys	Ser	Leu	Glu	Leu	Val	Ala	Thr	Ile	Asn	
			65					70					75		
Asn	Asn	Gly	Asp	Ser	Thr	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	
			80					85					90		
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	
			95					100					105		
Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Phe	Tyr	Cys	Ala	
			110					115					120		
Arg	Ala	Leu	Ile	Ser	Ser	Ala	Thr	Trp	Phe	Gly	Tyr	Trp	Gly	Gln	
			125					130					135		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
			140					145					150		
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	
			155					160					165		
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	
			170					175					180		
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
			185					190					195		
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	
			200					205					210		

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
215 220 225

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
230 235 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
245 250

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGGAGA 50
TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100
GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150
CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200
CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAGGATC AGCAGAGTGG 250
AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300
CTCACGTTTC GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350
ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu
1				5				10					15	
Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val
				20				25					30	
His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro
				35				40					45	
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe
				50				55					60	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
				65				70					75	
Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu
				80				85					90	
Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly	Ala
				95				100					105	
Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val
				110				115					120	
Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln	Leu	Lys				
				125				130						

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50
AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTCAGT AGCCACTACA 100
TGCACTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150
ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200
GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250

GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300
TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGCG CAGGGACCAC 350
GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400
CCATC 405

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu	Ile	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Met	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
Ser	His	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	35	40	45	
Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	65	70	75	
Ser	Ser	Thr	Ala	Asn	Val	His	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	80	85	90	
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	95	100	105	
Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	110	115	120	
Ser	Ser	Ala	Lys	Thr	Asp	Ser	Pro	Ile	Gly	Leu	Ser	Gly	Pro	Ile	125	130	135	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTTGGTGGAG GCGGAGGAGA CG 22

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50
TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100
TGCCTGTCAG TCTTGAGAT CAGGCCTCCA TCTCTTGCA ATCTAGTCAG 150
AGCCTTGATAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200
GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250
CTGGGGTCCC AGACAGGTTT AGTGGCAGTG GATCAGGGAC AGATTTTACA 300
CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350
TCAAAGTACA CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC 400
TGAAACGGGC TGTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450
GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500

CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTTAA 729

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Thr	20	25	30	
Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	35	40	45	
Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	50	55	60	
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	65	70	75	
Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	80	85	90	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	95	100	105	
Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	110	115	120	
His	Val	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	125	130	135	
Arg	Ala	Val	Ala	Ala	Pro	Thr	Val	Phe	Ile	Phe	Pro	Pro	Ser	Ser	140	145	150	
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	155	160	165	
Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	170	175	180	
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp				

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
1				5					10					15	
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Ile	Gln	Leu	Gln	Gln	Ser	
				20					25					30	
Gly	Pro	Glu	Leu	Met	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	
				35					40					45	
Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	
				50					55					60	
Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asp	
				65					70					75	
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	
				80					85					90	
Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Asn	Val	His	
				95					100					105	
Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	
				110					115					120	
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	
				125					130					135	
Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	
				140					145					150	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	
				155					160					165	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	
				170					175					180	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	
				185					190					195	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	
				200					205					210	
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	
				215					220					225	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	
				230					235					240	

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 245 250

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	1	5	10	15
Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	20	25	30	
His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	35	40	45	
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg	50	55	60	
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Asp	Ser	Gly	Ser	Gly	Thr	65	70	75	
Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	80	85	90	
Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly	95	100	105	
Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	110									

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	1	5	10	15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	20	25	30	
His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	35	40	45	
Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg	50	55	60	

Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 65 70 75
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 80 85 90
 Thr Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly
 95 100 105
 Gln Gly Thr Lys Val Glu Ile Lys Arg
 110

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Ile Ser
 20 25 30
 Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45
 Leu Leu Ile Tyr Tyr Ser Gly Ser Thr Leu Glu Ser Gly Val Pro
 50 55 60
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
 80 85 90
 Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val
 95 100 105
 Glu Ile Lys Arg

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly
 1 5 10 15

Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30
Ser	His	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	35	40	45
Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60
Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	65	70	75
Ser	Ser	Thr	Ala	Asn	Val	His	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	80	85	90
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	95	100	105
Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr				110	115	

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
Ser	His	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
Glu	Trp	Val	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
Asn	Gln	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	65	70	75	
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	95	100	105	
Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr				110	115		

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 Amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Thr	20	25	30	
Gly	His	Trp	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
Glu	Trp	Val	Gly	Met	Ile	His	Pro	Ser	Asp	Ser	Glu	Thr	Arg	Tyr	50	55	60	
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	65	70	75	
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Gly	Ile	Tyr	Phe	Tyr	Gly	95	100	105	
Thr	Thr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	110	115						

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	20	25	30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	50	55	60	
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	65	70	75	
Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	80	85	90	

Ser Gly Ser Gly	Ser Gly Thr Asp Phe	Thr Leu Thr Ile Ser Ser
95	100	105
Leu Gln Pro Glu	Asp Phe Ala Thr Tyr	Tyr Cys Ser Gln Ser Thr
110	115	120
His Val Pro Leu	Thr Phe Gly Gln Gly	Thr Lys Val Glu Ile Lys
125	130	135
Arg Thr Val Ala	Ala Pro Ser Val Phe	Ile Phe Pro Pro Ser Asp
140	145	150
Glu Gln Leu Lys	Ser Gly Thr Ala Ser	Val Val Cys Leu Leu Asn
155	160	165
Asn Phe Tyr Pro	Arg Glu Ala Lys Val	Gln Trp Lys Val Asp Asn
170	175	180
Ala Leu Gln Ser	Gly Asn Ser Gln Glu	Ser Val Thr Glu Gln Asp
185	190	195
Ser Lys Asp Ser	Thr Tyr Ser Leu Ser	Ser Thr Leu Thr Leu Ser
200	205	210
Lys Ala Asp Tyr	Glu Lys His Lys Val	Tyr Ala Cys Glu Val Thr
215	220	225
His Gln Gly Leu	Ser Ser Pro Val Thr	Lys Ser Phe Asn Arg Gly
230	235	240
Glu Cys		

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1 5 10 15
Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
20 25 30
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
35 40 45
Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
50 55 60
Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
65 70 75

Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	80	85	90
Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	95	100	105
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	110	115	120
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	125	130	135
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	140	145	150
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	155	160	165
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	170	175	180
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	185	190	195
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	200	205	210
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	215	220	225
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	230	235	240
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr			245	250	

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met	1	5	10	15
Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn	20	25	30	
Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	Asp	Ser	Val	Ala	Thr	35	40	45	
Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	Gly	Asp	Val	Ser	Gly	50	55	60	

Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	Phe	Ala	Gly	Ser	Ser	65	70	75
Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	Asn	Ser	Pro	Leu	80	85	90
Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	Pro	Gln	Ser	Val	95	100	105
Glu	Cys	Arg	Pro	Phe	Val	Phe	Ser	Ala	Gly	Lys	Pro	Tyr	Glu	Phe	110	115	120
Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	Gly	Val	Phe	Ala	125	130	135
Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	Phe	Ser	Thr	Phe	140	145	150
Ala	Asn	Ile	Leu	Arg	Asn	Lys	Glu	Ser							155		

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 780 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

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ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50
TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
TGTCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACTCTGGT ATCAACAGAA 200
ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

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TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser	20	25	30	
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	35	40	45	
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	50	55	60	
Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp	65	70	75	
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	80	85	90	
Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	95	100	105	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	110	115	120	
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	125	130	135	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	140	145	150	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	155	160	165	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	170	175	180	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	185	190	195	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu				

200	205	210
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
215	220	225
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
230	235	240
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
245	250	

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe		
1	5	10 15
Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser		
20	25	30
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr		
35	40	45
Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Ala Thr Tyr		
50	55	60
Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu		
65	70	75
Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe		
80	85	90
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser		
95	100	105
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr		
110	115	120
His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys		
125	130	135
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp		
140	145	150
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn		
155	160	165
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn		
170	175	180
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp		

185	190	195
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser		
200	205	210
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr		
215	220	225
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly		
230	235	240
Glu Cys		

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys
1 5 10 15
Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His
20 25 30
Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
35 40 45

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 780 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100

TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150

AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACACTGGT ATCAACAGAA 200

ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250

CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTTCACT 300

CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350

ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GGCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
 TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100
 AGGTTTCAGCT AGTGCACTCT GGCCTGCGCC TGGTGCAGCC AGGGGGCTCA 150
 CTCGGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCCTATAT 200
 GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
 TTGATCCTTC CAATGCTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300
 TTCACCTTAT CTCGCGACAA CTCCAAAAAC ACAGCATAAC TGCAGATGAA 350
 CAGCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400
 ATCGCTACAA TGGTGAATGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450
 GTCACCGTCT CCTCGGCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
 TCAAGGACTA CTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
 CTGACCAGCG GCGTGACAC CTTCCTGGCT GTCCTACAGT CCTCAGGACT 650
 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700

AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAAGTCGAC 750
AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800
CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850
TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900
CTCAAAAAGC TTGTCGGGGA GCGCTAA 927

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	20	25	30	
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	35	40	45	
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	50	55	60	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp	65	70	75	
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	80	85	90	
Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	95	100	105	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	110	115	120	
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	125	130	135	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	140	145	150	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	155	160	165	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	170	175	180	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	185	190	195	

His Thr Phe Pro	Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser	Leu
	200	205	210
Ser Ser Val Val	Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln	Thr
	215	220	225
Tyr Ile Cys Asn	Val Asn His Lys Pro	Ser Asn Thr Lys Val	Asp
	230	235	240
Lys Lys Val Glu	Pro Lys Ser Cys Asp	Lys Thr His Thr Cys	Pro
	245	250	255
Pro Cys Pro Ala	Pro Glu Leu Leu Gly	Gly Arg Met Lys Gln	Leu
	260	265	270
Glu Asp Lys Val	Glu Glu Leu Leu Ser	Lys Asn Tyr His Leu	Glu
	275	280	285
Asn Glu Val Ala	Arg Leu Lys Lys Leu	Val Gly Glu Arg	
	290	295	

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6563 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

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GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100
GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150
TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200
GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG 250
GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300
AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350
ATAGTCGCTT TGTTTTTATT TTTAATGTA TTTGTAATA GAATTCGAGC 400
TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450
ATCGCATTTT TTCTTGCATC TATGTTTCTT TTTTCTATTG CTACAAACGC 500
ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550
TGGGCGATAG GGTCACCATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600

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GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC 650
TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700
CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750
AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTTAC AGAGTACTCA 800
TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850
TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900
TCTGGAAGTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950
GGCCAAAGTA CAGTGGGAAGG TGGATAACGC CCTCCAATCG GGTAAGTCCC 1000
AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050
AGCACCTTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100
CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150
ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200
AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250
GAAAAAGAAT ATCGCATTTT TTCTTGATC TATGTTCTGT TTTTCTATTG 1300
CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG 1350
GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400
CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450
TGGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500
CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550
AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600
ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTGACGTC 1650
TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700
ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGACACAG 1750
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800
TCGTGGAACT CAGGCGCCTT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850
CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900
CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950
AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000
TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050

AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100
GAGAATGAAG TGGCAAGACT CAAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150
CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCGGCCGGGC GTTTTTTATT 2200
GTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT 2250
TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300
AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350
AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400
CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450
ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500
CCGCCGCCCA GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG 2550
CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600
GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650
CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700
CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750
GGCGCCATCT CCTTGACGC ACCATTCCCTT GCGGCGGCGG TGCTCAACGG 2800
CCTCAACCTA CTAAGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850
AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900
TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950
CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000
AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050
TTGGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC 3100
CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150
CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200
CCCATATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250
GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300
GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350
GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTGCGCATG 3400
GATTGTAGGC GCCGCCCTAT ACCTTGCTCT CCTCCCCGCG TTGCGTCGCG 3450

GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CCGCACCTCG 3500
 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550
 ACTGTGAATG CGCAAAACCA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600
 CATCTCCAGE AGCCGCACGC GCGCATCTC GGCAGCGTT GGGTCTTGGC 3650
 CACGGGTGCG CATGATCGTG CTCCTGTCTG TGAGGACCCG GCTAGGCTGG 3700
 CGGGGTTGCC TTA CTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750
 GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800
 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG 3850
 CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900
 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950
 TGATTTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCCTCA 4000
 CAACGTTCCA GTAACCGGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG 4050
 CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC 4100
 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA 4150
 TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200
 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250
 CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300
 AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350
 GCGGATGCCG GGAGCAGACA AGCCCGTCAG GCGCGTCAG CGGGTGTTGG 4400
 CGGGTGTCGG GCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450
 ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500
 ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550
 AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CCGTCGTTCG 4600
 GCTGCGGCGA GCGGTATCAG CTCACTCAAA GCGGGTAATA CCGTTATCCA 4650
 CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAAA AGGCCAGCAA 4700
 AAGGCCAGSA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750
 CCGCCCCCTT GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC 4800
 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850
 CTCGTGCGCT CTCCTGTTCC GACCCTGCGG CTTACCGGAT ACCTGTCCGC 4900

CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950
 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000
 CCCCCGTTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050
 GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100
 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150
 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200
 TCTGCTGAAG CCAGTTACTT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250
 GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG 5300
 ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350
 GGGGTCTGAC GCTCAGTGA ACGAAACTC ACGTTAAGGG ATTTTGGTCA 5400
 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA 5450
 AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA 5500
 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTGTT 5550
 CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG 5600
 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC 5650
 ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC 5700
 GCAGAAAGTG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT 5750
 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 5800
 TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG 5850
 CTTCATTCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC 5900
 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCTCTCGA TCGTTGTCAG 5950
 AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTATGGCA GCACTGCATA 6000
 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG 6050
 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 6100
 TTGCCCCGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA 6150
 AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC 6200
 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG 6250
 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG 6300

GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA 6350
 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 6400
 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA 6450
 TAGGGGTTCC GCGCACATTT CCCCAGAAAAG TGCCACCTGA CGTCTAAGAA 6500
 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC 6550
 CTTTCGTCTT CAA 6563

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	20	25	30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Glu	Thr	Tyr	50	55	60	
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	65	70	75	
Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	80	85	90	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	95	100	105	
Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	110	115	120	
His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	125	130	135	
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	140	145	150	
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	155	160	165	
Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	170	175	180	

Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
				185					190					195
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser
				200					205					210
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr
				215					220					225
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
				230					235					240
Glu	Cys													

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATGGTATAG GTTAACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CATGGTATAG GTNNSACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 780 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50
 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150

AGCTTAGTAC ATGGTATAGG TGAGACGTAT TTACTACTGGT ATCAACAGAA 200
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTAGTGCAGT CTGGCGGTGG CCTGGTGCAG CCAGGGGGCT CACTCCGTTT 50
 GTCCTGTGCA GCTTCTGGCT ACTCCTTC 78

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCGAGAAGGA GTAGCCAGAA GCTGCACAGG ACAAACGGAG TGAGCCCCCT 50
 GGCTGCACCA GGCCACCGCC AGACTGCACT AG 82

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8120 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG 50
GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 100
GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 150
TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 200
GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 250
CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 300
TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 350
AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 400
CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA 450
GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT 500
TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAATATG GGGATTGGCA 550
AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC 600
CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAACAGA ATCTGGTGAT 650
TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA 700
AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA 750
GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCTTAA GACTTATTGA 800
ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA 850
GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT 900
GTGACAAGGA TCATGCAGGA ATTTGAAAGT GACACGTTTT TCCCAGAAAT 950
TGATTTGGGG AAATATAAAC CTCTCCCAGA ATACCAGGC GTCCTCTCTG 1000
AGTCCAGGA GGAAAAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGAAG 1050
AAAGACTAAC AGGAAGATGC TTTCAAGTTC TCTGCTCCCC TCCTAAAGCT 1100
ATGCATTTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCCTTGG 1150

CTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATACAC 1200
 ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA 1250
 CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT 1300
 CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT 1350
 GGAGTACATT CAGAAGTTCA GCTAGTGACG TCTGGCGGTG GCCTGGTGCA 1400
 GCCAGGGGGC TCACTCCGTT TGTCTGTGC AGCTTCTGGC TACTCCTTCT 1450
 CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCAGGTAA GGCCTGGAA 1500
 TGGGTTGGAT ATATTGATCC TTCCAATGGT GAAACTACGT ATAATCAAAA 1550
 GTTCAAGGGC CGTTTCACTT TATCTCGCGA CAACTCCAAA AACACAGCAT 1600
 ACCTGCAGAT GAACAGCCTG CGTGCTGAGG AACTGCCGT CTATTACTGT 1650
 GCAAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG 1700
 TCAAGGAACC CTGGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG 1750
 TCTTCCCCCT GGCACCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC 1800
 CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG 1850
 GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC 1900
 AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGAAGT GTCCCTCTAGC 1950
 AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA 2000
 CACCAAGGTG GACAAGAAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA 2050
 CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC 2100
 CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA 2150
 GGTACATGC GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT 2200
 TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAAGCCG 2250
 CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT 2300
 CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA 2350
 ACAAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCA AGCCAAAGGG 2400
 CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCCATCCC GGGAAGAGAT 2450
 GACCAAGAAC CAGGTACGCC TGACCTGCCT GGTCAAAGGC TTCTATCCA 2500
 GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACCTAC 2550
 AAGACCACGC CTCCCGTCTT GGAATCCGAC GGTCTCTTCT TCCTCTACAG 2600

CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT 2650
 GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC 2700
 TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA 2750
 AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA 2800
 AATAAAGCAA TAGCATCACA AATTTACAAA ATAAAGCATT TTTTTCCTG 2850
 CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG 2900
 GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT 2950
 GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG 3000
 GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 3050
 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 3100
 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 3150
 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 3200
 CGCCCAAGTC CGCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 3250
 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 3300
 AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 3350
 CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA 3400
 GTACCGCCTA TAGAGTCTAT AGGCCACCCC CCTTGGCTTC GTTAGAACGC 3450
 GGCTACAATT AATACATAAC CTTTGGATC GATCCTACTG AACTGACAT 3500
 CCACTTTTTT TTTTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC 3550
 TCGGTTGCGG AAGCTAGCTT GGGCTGCATC GATTGAATTC CACCATGGGA 3600
 TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC 3650
 AGATATCCAG ATGACCCAGT CCCCAGCTC CCTGTCCGCC TCTGTGGGCG 3700
 ATAGGGTCAC CATCACCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA 3750
 GGTGCTACGT ATTTACACTG GTATCAACAG AAACCAGGAA AAGCTCCGAA 3800
 ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT 3850
 TCTCTGGATC CGGTTCTGGG ACGGATTTC A CTCTGACCAT CAGCAGTCTG 3900
 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC 3950
 GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG 4000

CACCATCTGT CTTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA 4050
 ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA 4100
 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA 4150
 GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC 4200
 CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA 4250
 AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG 4300
 GAGAGTGTTA AGCTTGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT 4350
 AATGGTTACA AATAAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT 4400
 TTTTTCCTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT 4450
 ATCATGTCTG GATCATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA 4500
 AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA 4550
 ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC 4600
 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG 4650
 GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC 4700
 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG 4750
 CCCCTAACTC CGCCAGTTC CGCCATTCT CCGCCCCATG GCTGACTAAT 4800
 TTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC 4850
 AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTG 4900
 TTACCTCGAG CGGCCGCTTA ATTAAGGCGC GCCATTTAAA TCCTGCAGGT 4950
 AACAGCTTGG CACTGGCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC 5000
 TGGCGTTACC CAACTTAATC GCCTTGACAGC ACATCCCCC TTCGCCAGCT 5050
 GGCCTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT 5100
 AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT 5150
 GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACBCGCCCTG 5200
 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG 5250
 CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCTTCC 5300
 TTTCTCGCCA CGTTCGCCG CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT 5350
 CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC 5400
 TTGATTTGGG TGATGGTTCA CGTAGTGGGC CATCGCCCTG ATAGACGGTT 5450

TTTCCGCCCTT TGACGTTGGA GTCCACGTTT TTTAATAGTG GACTCTTGTT 5500
 CCAAACCTGGA ACAACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT 5550
 AAGGGATTTT GCCGATTTTCG GCCTATTGGT TAAAAAATGA GCTGATTTAA 5600
 CAAAAATTTA ACGCGAATTT TAACAAAATA TTAACGTTTA CAATTTTATG 5650
 GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAACTCC 5700
 GCTATCGCTA CGTGA CTGGG TCATGGCTGC GCGCCGACAC CCGCCAACAC 5750
 CCGCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGGCATC CGCTTACAGA 5800
 CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCACCGTC 5850
 ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA 5900
 TACGCTTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG 5950
 TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 6000
 TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT 6050
 AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTT 6100
 CGTGTGCCCC TTATTCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC 6150
 TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG 6200
 CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG 6250
 AGTTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT 6300
 GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG 6350
 GTCGCCGCAT AACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC 6400
 ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 6450
 TGCCATAACC ATGAGTGATA AACTGCGGC CAACTTACTT CTGACAACGA 6500
 TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT 6550
 GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA 6600
 CGACGAGCGT GACACCACGA TGCCAGCAGC AATGGCAACA ACGTTGCGCA 6650
 AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA 6700
 GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 6750
 TCCGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGCT GAGCGTGGGT 6800
 CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC 6850

GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG 6900
 ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG 6950
 ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA 7000
 TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT 7050
 CCCTTAACGT GAGTTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA 7100
 TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG 7150
 CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA 7200
 GCTACCAACT CTTTTTCCGA AGGTAAC TGG CTTCAGCAGA GCGCAGATAC 7250
 CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 7300
 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAAGTGGC 7350
 TGCTGCCAGT GGCATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT 7400
 AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TCGTGACACA 7450
 CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG 7500
 TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAAG GCGGACAGGT 7550
 ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 7600
 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 7650
 ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA 7700
 AAAACGCCAG CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT 7750
 TTTGCTCACA TGTTCTTTCC TGCGTTATCC CCTGATTCTG TGGATAACCG 7800
 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGACG CGAACGACCG 7850
 AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAA 7900
 CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATCCAGCT GGCACGACAG 7950
 GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT 8000
 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT 8050
 ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTACACAG GAAACAGCTA 8100
 TGACCATGAT TACGAATTAA 8120

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 800 base pairs
 - (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
TCTTCTTGCA TCTATGTTGG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100
AGGTTTCAGCT AGTGCACTCT GCGGTGGGCC TGGTGCAGCC AGGGGGCTCA 150
CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200
GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300
TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATAACC TGCAGATGAA 350
CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400
ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450
GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
TCAAGGACTA CTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650
CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700
AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750
AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCTGA 800

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
1					5				10					15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser
					20				25					30
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
					35				40					45
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val

	20	25	30
Ser His Tyr Met	His Trp Val Arg Gln Ala	Pro Gly Lys Gly Leu	
	35	40	45
Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr		55	60
	50		
Asn Gln Lys Phe Lys Gly Arg Phe Thr Leu Ser Arg Asp Asn Ser		70	75
	65		
Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp		85	90
	80		
Thr Ala Val Tyr Tyr Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly		100	105
	95		
Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val		115	120
	110		
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro		130	135
	125		
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu		145	150
	140		
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser		160	165
	155		
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		175	180
	170		
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser		190	195
	185		
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys		205	210
	200		
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		220	225
	215		
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu		235	240
	230		
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		250	255
	245		
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp		265	270
	260		
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp		280	285
	275		
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln		295	300
	290		
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His			

305	310	315
Gln Asp Trp Leu Asn Gly Lys Glu Tyr	Lys Cys Lys Val Ser Asn	
320	325	330
Lys Ala Leu Pro Ala Pro Ile Glu Lys	Thr Ile Ser Lys Ala Lys	
335	340	345
Gly Gln Pro Arg Glu Pro Gln Val Tyr	Thr Leu Pro Pro Ser Arg	
350	355	360
Glu Glu Met Thr Lys Asn Gln Val Ser	Leu Thr Cys Leu Val Lys	
365	370	375
Gly Phe Tyr Pro Ser Asp Ile Ala Val	Glu Trp Glu Ser Asn Gly	
380	385	390
Gln Pro Glu Asn Asn Tyr Lys Thr Thr	Pro Pro Val Leu Asp Ser	
395	400	405
Asp Gly Ser Phe Phe Leu Tyr Ser Lys	Leu Thr Val Asp Lys Ser	
410	415	420
Arg Trp Gln Gln Gly Asn Val Phe Ser	Cys Ser Val Met His Glu	
425	430	435
Ala Leu His Asn His Tyr Thr Gln Lys	Ser Leu Ser Leu Ser Pro	
440	445	450
Gly Lys		

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val	
1	15
Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val	
20	30
His Gly Ile Gly Ala Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro	
35	45
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe	
50	60
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
65	75
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr	

	80	85	90
Tyr Tyr Cys Ser Gln Ser Thr His Val	95	100	105
Gly Thr Lys Val Glu Ile Lys Arg Thr	110	115	120
Phe Ile Phe Pro Pro Ser Asp Glu Gln	125	130	135
Ser Val Val Cys Leu Leu Asn Asn Phe	140	145	150
Val Gln Trp Lys Val Asp Asn Ala Leu	155	160	165
Glu Ser Val Thr Glu Gln Asp Ser Lys	170	175	180
Ser Ser Thr Leu Thr Leu Ser Lys Ala	185	190	195
Val Tyr Ala Cys Glu Val Thr His Gln	200	205	210
Thr Lys Ser Phe Asn Arg Gly Glu Cys	215		